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|----------------|------------|---|-------------------------------|---|--------|-----------|------|---------|
| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM | Book |
| Search Protein | | <input checked="" type="checkbox"/> for | | | | | Go | Clear |
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☐ 1: BAA91568. unnamed protein p...[gi:7022355] BLink, Nucleotide, Related Sequences, Taxonomy, LinkOut

LOCUS BAA91568 634 aa linear PRI 22-FEB-2000
 DEFINITION unnamed protein product [Homo sapiens].
 ACCESSION BAA91568
 PID g7022355
 VERSION BAA91568.1 GI:7022355
 DBSOURCE locus AK001230 accession [AK001230.1](#)
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
 Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
 Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
 Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
 Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
 Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
 Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished (2000)
 REFERENCE 2 (residues 1 to 634)
 AUTHORS Isogai,T. and Otsuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing and clone selection:
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.
 FEATURES
 source Location/Qualifiers
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 /clone_lib="NT2RM2"
 /note="cloning vector: pME18SFL3; mRNA from uninduced NT2
 neuronal precursor cells."
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 CDS 1..634
 /coded_by="AK001230.1:24..1928"
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241 iyslhtklqs mnsenqtmls lefhlhggtg ygrgirvlpe snsdrvdlkk dlesanltan
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Revised: October 24, 2001.

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Comparison
w/
SeqIDNO: 13

248-13.rspt

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Query Match          99.8%; Score 3317; DB 4; Length 634;
Best Local Similarity 99.8%; Pred. No. 4.2e-265;
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCVQPMQYFDLTCQLLGKAEVDGASFL 180
QY 181 LKVDGTRTPFPFSWRVLIQDLVLEGDLSHIHRLQNLTDILVYDNHVVHVARSLKVGSLR 240
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Db 301 QHSDVICQSEPDDSFPSGVSLSYEVERCQQLSATILTDHQYLERTPLCAILKQKAPQQY 360
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Db 361 RIRAKLSYKPRRLFQSVKLHCPKCHLLQEVPHGEDLDIIFQDGATKTPVVKLQNTSLYD 420
QY 421 SKIWTTKNQKGRKVAHVHVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGH 480
Db 421 SKIWTTKNQKGRKVAHVHVKNNGILPLSNECLLLIEGGTLSEICKLSNKFNSVIPVRSGH 480
QY 481 EDLELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQY 540
Db 481 EDLELLDLSAPFLIQGTIHHYGCKQCSSLRSIQNLNSLVDKTSWIPSSVAEALGIVPLQY 540
QY 541 VFVMTFTLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMMIMDMFCPPGIKIDAY 600
Db 541 VFVMTFTLDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMMIMDMFCPPGIKIDAY 600
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RESULT 3

Compass 49
SERIDNO: 17

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Matches 503; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Db    121 KYFNFTTEDHKMVEALRVWASTHMSPSWTLLKLCVQPMQYFDLTCQLLGKAEVDGASFL 180
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Db    181 LKVWDGTRTPFPSPWRVLIQDLVLEGLDSHRLQNLTDILVYDNHVVHVARSLKVGSLR 240
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Db    301 QHSDVICQSEPDDSFPSGVSLSYEVERCQQLSATILTDHQYLERTPLCAILKQKAPQY 360
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Db    361 RIRAKLSYKPRRLFQSVKLHCPKCHLLQEVPHGEDLDIIFQDGATKTPDVKLQNTSLYD 420
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Comparison: SIB ID 20:15

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QY 61 LFSGNTREALPIIYKNGDIYVFRHLKIQVYKKEGITS SGFASLTFEGTLGAPILPRTSS 120
DB 61 LFSGNTREALPIIYKNGDIYVFRHLKIQVYKKEGITS SGFASLTFEGTLGAPILPRTSS 120
QY 121 KYNFTTDEHKVVEALRVNASTHSPSWTLKLCQVPMQYFDLTCQLLGAKEVDGASFL 180
DB 121 KYNFTTDEHKVVEALRVNASTHSPSWTLKLCQVPMQYFDLTCQLLGAKEVDGASFL 180
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DB 181 LKVMQGTPTPPSWRVLIQDVLLEGDLSHIRLQNLITIDILVYDNHVAHSLKYGSPFLR 240

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QY 301 QHSDVICOSEPPDDSEFPNGVSL 321
DB 301 QHSDVICOSEPPDDSEFPNGVSL 321